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<110> Gurney, Mark  
Bienkowski, Michael J.

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Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45  
  
Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60  
  
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80  
  
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95  
  
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110  
  
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125  
  
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140  
  
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160  
  
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175  
  
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190  
  
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro  
195 200 205  
  
Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220  
  
Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240  
  
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255  
  
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala  
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp  
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp  
485 490 495

Ile Ser Leu Leu Lys  
500

<210> 9  
<211> 2088  
<212> DNA  
<213> Homo sapiens

<400> 9  
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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120  
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
acctgcattt ataccaagga aggcatctg cagtatggcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtgcacac ccattccccac tttgtgattt cctaccgctg ctttagtttgtt 360  
gagttgttaa gtgatgcct tctcggtt gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaaattga caagttccga 540  
ggggtagagt ttgtgttgtt cccactggct gaagaaaatgt acaatgttgg 600

gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg 660  
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720  
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgagga 780  
ccctacgaag aagccacaga gagaaccacc agcattcca ccaccaccac caccaccaca 840  
gagtctgtgg aagaggtggt tcgagttcct acaacacgag ccagtacccc tgatgccgtt 900  
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccattcca gaaagccaaa 960  
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020  
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080  
caggagaaag tggaatctt ggaacaggaa gcagccaacg agagacagca gctgggtggag 1140  
acacacatgg ccagagtgga agccatgtc aatgacgcgc gccgcctggc cctggagaac 1200  
tacatcaccg ctctgcaggc tggcctcct cggcctcgac acgtgttcaa tatgctaaag 1260  
aagtatgtcc ggcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320  
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gtcttggcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560  
tcttgaccg aaacgaaaac caccgtggag ctccctcccg tgaatggaga gttcagcctg 1620  
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gaagttgagc ctgttgatgc ccgcctgtc gccgaccgag gactgaccac tcgaccaggt 1740  
tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcaagattc 1800  
cgacatgact cagatatga agttcatcat caaaaattgg tggccttgc agaagatgtg 1860  
ggttcaaaca aaggtgcaat cattggactc atggtggcg gtgttgtcat agcgacagtg 1920  
atcgcatca cttgggtat gctgaagaag aaacagtaca catccattca tcatgggttg 1980  
gtggaggtt acgcccgtt caccggcag gagcgccacc tgtccaagat gcagcagaac 2040  
ggctacgaaa atccaaccta caagttctt gagcagatgc agaactag 2088

<210> 10  
<211> 695  
<212> PRT  
<213> Homo sapiens

<400> 10  
Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30  
  
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

<210> 11  
<211> 2088  
<212> DNA  
<213> Homo sapiens

<400> 11  
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cccaactgatg gtaatgctgg cctgctggct gaaccccaga ttgcctatgtt ctgtggcaga 120  
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtgcaagac ccattccccac tttgtgattc cctaccgctg ctttagtttgt 360  
gagtttgtaa gtgatgcct tctcgttccct gacaagtgca aattcttaca ccaggagagg 420  
atggatgttt gcgaaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtagcca acttgcataa ctacggcatg ttgctgccct gcggaaattga caagttccga 540  
gggttagagt ttgtgtgtt cccactggct gaagaaaatg acaatgtgga ttctgctgat 600  
gcggaggagg atgactcgga tgtctgggtt ggcggagcag acacagacta tgcagatggg 660  
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720  
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840  
gagtctgtgg aagaggttgt tcgagttccct acaacagcag ccagtacccc tgatgccgtt 900  
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960

gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atggaaagag 1020  
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080  
caggagaaag tggaatctt ggaacagggaa gcagccaaacg agagacagca gctggtag 1140  
acacacatgg ccagagtggc agccatgctc aatgaccgccc gccgcctggc cctggagaac 1200  
tacatcaccg ctctgcaggc tgccctcgct cggcctcgct acgtgttcaa tatgttaaag 1260  
aagtatgtcc ggcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320  
cgcatggtg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt 1380  
gtgatttatg agcgcatgaa tcagtctctc tccctgtct acaacgtgcc tgcagtggcc 1440  
gaggagattc agatgaagt tgatgagctg cttcagaaag agcaaaaacta ttcatgac 1500  
gtcttggcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560  
tctttgaccg aaacgaaaac caccgtggag ctccttccc tgaatggaga gttcagcctg 1620  
gacgatctcc agccgtggca ttctttggg gctgactctg tgccagccaa cacagaaaac 1680  
gaagttgagc ctgttgatgc cgcgcctgct gccgaccgag gactgaccac tcgaccaggt 1740  
tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc 1800  
cgacatgact cagggatatga agttcatcat caaaaattgg tgcccttgc agaagatgtg 1860  
ggttcaaaca aaggtgcaat cattggactc atggtggcg gtgttgtcat agcgcacagt 1920  
atcgcatca cttgggtgat gctgaagaag aaacagtaca catccattca tcatgggttg 1980  
gtggaggttgc acggcgctgt caccggcagag gagcgccacc tgtccaagat gcagcagaac 2040  
ggctacgaaa atccaaccta caagttctt gagcagatgc agaactag 2088

<210> 12

<211> 695

<212> PRT

<213> Homo sapiens

<400> 12

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

<210> 13  
<211> 2088  
<212> DNA  
<213> Homo sapiens

<400> 13  
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtgcacac ccacccac tttgtgattc cttaccgctg cttagtttgt 360  
gagtttgtaa gtgatgccct tctcgccct gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcacca ctacggcatg ttgctgccct gcggaaattga caagttccga 540  
ggggtagagt ttgtgtgtt cccactggct gaagaaagtg acaatgtgga ttctgctgat 600  
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gaagccgatg atgacgagga cgatgaggat ggtatgagg tagaggaaga ggctgaggg 780  
ccctacgaag aagccacaga gagaaccacc agcattgcc ccaccaccac caccaccaca 840  
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tacatcacccg ctctgcaggc tgttcctcct cggcctcgac acgtgttcaa tatgctaaag 1260  
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gaagttgagc ctgttgatgc ccgcctgtct gccgaccgag gactgaccac tcgaccagg 1740  
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cgacatgact cagggatatga agttcatcat caaaaattgg tgttcttgc agaagatgtg 1860  
ggttcaaaca aaggtgcaat cattggactc atggtggcg gtgttgtcat agcgacagt 1920  
atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcattgtgt 1980  
gtggaggttg acgcccgtgt cacccccagag gagcgccacc tgtccaagat gcagcagaac 2040  
ggctacgaaa atccaaccta caagttctt gagcagatgc agaactag 2088

<210> 14  
<211> 695  
<212> PRT  
<213> Homo sapiens

<400> 14  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

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<211> 2094  
<212> DNA  
<213> Homo sapiens

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gggttagagt ttgtgtgtt cccactggct gaagaaagtg acaatgtgga ttctgctgat 600  
gcggaggagg atgactcgga tgtctgggtt ggcggagcag acacagacta tgcagatggg 660  
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<210> 16

<211> 697

<212> PRT

<213> Homo sapiens

<400> 16

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

<210> 17

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 17

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
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gagtttgtaa gtgatgcctt ttcgttccct gacaagtgc aattcttaca ccaggagagg 420  
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gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagagaaga ggctgaggaa 780  
ccctacgaag aagccacaga gagaaccacc agcattgcc ccaccaccac caccaccaca 840  
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<211> 697  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

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<211> 2094  
<212> DNA  
<213> Homo sapiens

<400> 19

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<211> 697

<212> PRT

<213> Homo sapiens

<400> 20

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35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

<210> 21

<211> 1341

<212> DNA

<213> Homo sapiens

<400> 21

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gacgaagagc ccgaggagcc cggccggagg ggcagcttg tggagatggt ggacaacctg 180  
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ctcaacatcc tggtggtatac aggcagcagt aactttgcag tgggtgctgc cccccacccc 300  
ttcctgcattc gctactacca gaggcagctg tccagcacat accgggaccc cggaaagggt 360  
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cccaacctct tctccctgca cctttgtggt gctggcttc ccctcaacca gtctgaagt 660  
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acggcagcgg tggaggccc ttttgtcacc ttggacatgg aagactgtgg ctacaacatt 1320  
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<210> 22

<211> 446

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln  
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His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu  
20 25 30

Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly  
35 40 45

Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser  
50 55 60

Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr  
65 70 75 80

Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala  
85 90 95

Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser  
100 105 110

Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly  
115 120 125

Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly  
130 135 140

Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp  
145 150 155 160

Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala  
165 170 175

Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp  
180 185 190

Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu  
195 200 205

Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val  
210 215 220

Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly  
225 230 235 240

Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile  
245 250 255

Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys  
260 265 270

Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu  
275 280 285

Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala  
290 295 300

Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln  
305 310 315 320

Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val  
325 330 335

Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile  
340 345 350

Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr  
355 360 365

Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly  
370 375 380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp  
385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His  
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp  
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
435 440 445

<210> 23

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 23

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ggggcgccc ccctggggct gcggctgccc cgggagaccg acgaagagcc cgaggagccc 180  
ggccggaggg gcagctttgt ggagatggtg gacaacctga ggggcaagtc ggggcagggc 240  
tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca 300  
ggcagcagta actttgcagt ggggtgctgcc cccccacccct tcctgcatacg ctactaccag 360  
aggcagctgt ccagcacata ccggggacctc cggaagggtg tgtatgtgcc ctacacccag 420  
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actgtgcgtg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc 540  
aactgggaag gcatcctggg gctggcctat gctgagattg ccaggcctga cgactccctg 600  
gagcctttct ttgactctct ggtaaagcag acccacgttc ccaacacctt ctcctgcac 660  
ctttgtggtg ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggagggagc 720  
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cggcgggagt ggtattatga ggtcatcatt gtgcgggtgg agatcaatgg acagatctg 840  
aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac 900  
cttcgtttgc ccaagaaagt gtttgaagct gcagtcaaat ccatcaaggc agcctcctcc 960  
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<210> 24

<211> 459

<212> PRT

<213> Homo sapiens

<400> 24

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr  
1 5 10 15

Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile  
20 25 30

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg  
35 40 45

Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly  
50 55 60

Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly  
65 70 75 80

Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile  
85 90 95

Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His  
100 105 110

Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg  
115 120 125

Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu  
130 135 140

Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val  
145 150 155 160

Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe  
165 170 175

Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu  
180 185 190

Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val  
195 200 205

Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala  
210 215 220

Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser  
225 230 235 240

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp  
245 250 255

Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg  
260 265 270

Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn  
275 280 285

Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro  
290 295 300

Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser  
305 310 315 320

Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys  
325 330 335

Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu  
340 345 350

Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu  
355 360 365

Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp  
370 375 380

Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met  
385 390 395 400

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg  
405 410 415

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe  
420 425 430

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp  
435 440 445

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
450 455

<210> 25

<211> 1302

<212> DNA

<213> Homo sapiens

<400> 25

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gtggagatgg tggacaaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180  
gtgggcagcc ccccgagac gctcaacatc ctggtgata caggcagcag taactttgca 240  
gtgggtgctg cccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 300  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 360  
ctgggcaccc acctggtaag catccccat ggccccaacg tcactgtgc tgccaaacatt 420  
gctgccatca ctgaatcaga caagtttttc atcaacggct ccaactggga aggcatcctg 480  
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccctt ctttgactct 540  
ctggtaaagc agacccacgt tcccaaccc ttctccctgc acctttgtgg tgctggcttc 600  
cccctcaacc agtctgaagt gctggcctt gtcggaggaa gcatgatcat tggaggtatc 660  
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggattat 720  
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatggg ctgcaaggag 780  
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgtt gcccaagaaa 840  
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 900  
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catgtgcacg atgagtttag gacggcagcg gtggaaaggcc cttttgtcac cttggacatg 1260  
gaagactgtg gctacaacat tccacagaca gatgagtcata 1302

<210> 26

<211> 433

<212> PRT

<213> Homo sapiens

<400> 26

Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly  
1 5 10 15

Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu  
20 25 30

Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg  
35 40 45

Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro  
50 55 60

Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala  
65 70 75 80

Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln  
85 90 95

Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr  
100 105 110

Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile  
115 120 125

Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr  
130 135 140

Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu  
145 150 155 160

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro  
165 170 175

Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser  
180 185 190

Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu  
195 200 205

Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu  
210 215 220

Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr  
225 230 235 240

Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met  
245 250 255

Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr  
260 265 270

Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser  
275 280 285

Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu  
290 295 300

Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile  
305 310 315 320

Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser  
325 330 335

Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp  
340 345 350

Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser  
355 360 365

Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val  
370 375 380

Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys  
385 390 395 400

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val  
405 410 415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu  
420 425 430

Ser

<210> 27  
<211> 1278  
<212> DNA  
<213> Homo sapiens

<400> 27  
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ggcaagtccgg ggcagggcta ctacgtggag atgaccgtgg gcagcccccc gcagacgctc 180  
aacatcctgg tggatacagg cagcagtaac tttgcagtgg gtgctgcccc ccaccccttc 240  
ctgcatcgct actaccagag gcagctgtcc agcacatacc gggacctccg gaagggtgtg 300  
tatgtgccct acacccaggg caagtggaa gggagctgg gcacccgaccc ggttaagcattc 360  
ccccatggcc ccaacgtcac tgtgcgtgcc aacattgctg ccatcaactga atcaagacaag 420  
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ctctggtata caccatccg gcgggagtggtt tattatgagg tcatttcattgt gcgggtggag 720  
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gacagtggca ccaccaacct tcgtttgccc aagaaaagtgt ttgaagctgc agtcaaatcc 840  
atcaaggcag cctcctccac ggagaagttc cctgatggtt tctggctagg agagcagctg 900  
gtgtgctggc aaggcaggcac cacccttgg aacattttcc cagtcatttc actctaccta 960  
atgggtgagg ttaccaacca gtccttccgc atcaccatcc ttccgcagca atacctgcgg 1020  
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tccacgggca ctgttatggg agctgttatac atggagggtt tctacgttgt ctgtatcgg 1140  
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cagacagatg agtcatgt 1278

<210> 28  
<211> 425  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr  
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Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe  
20 25 30  
  
Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr  
35 40 45  
  
Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val  
50 55 60  
  
Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe  
65 70 75 80  
  
Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu  
85 90 95  
  
Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu  
100 105 110  
  
Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val  
115 120 125  
  
Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn  
130 135 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala  
145 150 155 160

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln  
165 170 175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe  
180 185 190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile  
195 200 205

Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr  
210 215 220

Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu  
225 230 235 240

Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp  
245 250 255

Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys  
260 265 270

Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu  
275 280 285

Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln  
290 295 300

Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu  
305 310 315 320

Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln  
325 330 335

Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys  
340 345 350

Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala  
355 360 365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg  
370 375 380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr  
385 390 395 400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly  
405 410 415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
420 425

<210> 29  
<211> 1362  
<212> DNA  
<213> Homo sapiens

<400> 29  
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ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgcc cccccctgggg 120

ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagctt 180  
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gtgggcagcc ccccgcagac gctcaacatc ctggtgata caggcagcag taactttgca 300  
gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccc acctggtaag catccccat ggccccaaacg tcactgtcg tgccaaacatt 480  
gctgccatca ctgaatcaga caagtttttc atcaacggct ccaactggga aggcatcctg 540  
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ctggtaaagc agacccacgt tcccaaccc ttctccctgc acctttgtgg tgctggcttc 660  
cccctaacc agtctgaagt gctggcctt gtcggaggg gcatgatcat tggaggtatc 720  
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggatttat 780  
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840  
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgtt gcccaagaaa 900  
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960  
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ttcccagtca tctcactcta cctaattgggt gaggttacca accagtcctt ccgcacatcacc 1080  
atccttccgc agcaataacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140  
tacaagtttgc ccatctcaca gtcatccacg ggcactgtt tggagctgt tatcatggag 1200  
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catgtgcacg atgagttcag gacggcagcg gtggaaaggcc cttttgtcac cttggacatg 1320  
gaagactgtg gctacaacat tccacagaca gatgagtcata ga 1362

<210> 30

<211> 453

<212> PRT

<213> Homo sapiens

<400> 30

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser  
450

<210> 31  
<211> 1380

<212> DNA

<213> Homo sapiens

<400> 31

atggcccaag ccctgccctg gtcctgtcg tggatggcg cgggagtgc gcctgcccac 60

ggcacccagc acggcatccg gctgcccctg cgtagcggcc tggggggcgc cccctgggg 120  
ctcggtgc cccggagac cgacgaagag cccgaggagc ccggccggag gggcagctt 180  
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc ccccgagac gctcaacatc ctggtgata caggcagcag taactttgca 300  
gtgggtgctg cccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccc acctggtaag catccccat ggccccaacg tcactgtgc tgccaaacatt 480  
gctgccatca ctgaatcaga caagtttttc atcaacggct ccaactggga aggcatcctg 540  
gggctggcct atgctgagat tgccaggcct gacgactccc tggagcctt ctttactct 600  
ctggtaaagc agacccacgt tcccaacetc ttctccctgc acctttgtgg tgctggcttc 660  
cccctcaacc agtctgaagt gctggcctct gtcggaggg gcatgatcat tggaggtatc 720  
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggattat 780  
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatggg ctgcaaggag 840  
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgtt gcccaagaaa 900  
gtgttgaag ctgcagtcaa atccatcaag gcagcctct ccacggagaa gttccctgat 960  
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020  
ttcccaagtca tctcaactcta cctaattgggt gaggttacca accagtcctt ccgcattcacc 1080  
atccttccgc agcaataacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140  
tacaagtttgc ccatctcaca gtcattccacg ggcactgtt tggagctgt tatcatggag 1200  
ggcttctacg ttgtctttga tcggggccga aaacgaattt gctttctgt cagcgcttgc 1260  
catgtgcacg atgagttcag gacggcagcg gtggaaaggcc ctttgtcac cttggacatg 1320  
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga 1380

<210> 32

<211> 459

<212> PRT

<213> Homo sapiens

<400> 32

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser His His His His His His  
450 455

<210> 33

<211> 25

<212> PRT

<213> Homo sapiens

<400> 33

- 40 -

Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu  
1 5 10 15

Ser Ser Leu Val Arg His Arg Trp Lys  
20 25

<210> 34  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 34  
Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser  
1 5 10 15

Leu Leu Lys

<210> 35  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 35  
gtggatccac ccagcacggc atccggctg 29

<210> 36  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 36  
gaaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 37  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 37  
gatcgatgac tatctctgac tctccgcgtg aacaggacg 39

<210> 38  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 38  
gatccgtcct gttcacgcgg agagtcagag atagtcatc 39

<210> 39  
<211> 77  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2

<400> 39  
cggcatccgg ctgcccctgc gtagcggtct gggtggtgct ccactgggtc tgcgtctgcc 60  
ccgggagacc gacgaag 77

<210> 40  
<211> 77  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2

<400> 40  
cttcgtcggt ctccccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60  
ggggcagccg gatgccg 77

<210> 41  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 41  
gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Caspase 8  
Cleavage Site

<400> 42  
gatccgtcgg tttcgataacc agagtccagc ggagagtcag agatagtcat c 51

<210> 43  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 43  
aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 44  
gaaagcttc atgactcatc tgtctgtgga atgttg 36

<210> 45  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: 6-His tag

<400> 45  
gatcgcatca tcaccatcac` catg 24

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: 6-His tag  
  
<400> 46  
gatccatggt gatggtgatg atgc 24  
  
<210> 47  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 47  
gactgaccac tcgaccagg t c 22  
  
<210> 48  
<211> 51  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 48  
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51  
  
<210> 49  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 49  
cgaattaaat tccagcacac tggcta 26  
  
<210> 50  
<211> 1287  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Hu-Asp2 (b)  
delta TM  
  
<400> 50  
atggcccaag ccctgccctg gtcctgctg tggatggcg cgaggagtgt gcctgcccac 60  
ggcacccagc acggcatccg gtcgcctcg cgcagccgc tggggggcgc cccctgggg 120  
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagctt 180  
gtggagatgg tggacaacct gagggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc cccgcagac gtcacacatc ctggtgata caggcagcag taactttgca 300  
gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccg acctggtaag catccccat ggccccaacg tcactgtgcg tgccaacatt 480  
gctgccatca ctgaatcaga caagttttc atcaacggct ccaactggga aggcatcctg 540

gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600  
gaagtgtcg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660  
acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720  
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtagaa ctatgacaag 780  
agcattgtgg acagtggcac caccaacctt cgtttgcac agaaagtgtt tgaagctgca 840  
gtcaaattcca tcaaggcagc ctcctccacg gagaagttcc ctgatggtt ctggctagga 900  
gagcagctgg tgtgctggca agcaggcacc accccttggaa acattttccc agtcatctca 960  
ctctacctaa tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa 1020  
tacctgcggc cagtggaaata tggccacg tcccaagacg actgttacaa gtttgcac 1080  
tcacagtcat ccacgggcac tgttatggaa gctgttatca tggaggcgtt ctacgttgtc 1140  
tttgcggc cccgaaaacg aattggctt gctgtcagcg cttgccatgt gcacgatgag 1200  
ttcaggacgg cagcgggtgaa aggcccttt gtcaccccttgg acatggaaga ctgtggctac 1260  
aacattccac agacagatga gtcatga 1287

<210> 51  
<211> 428  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2 (b)  
delta TM

<400> 51  
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15  
  
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30  
  
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45  
  
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60  
  
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80  
  
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95  
  
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110  
  
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125  
  
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140  
  
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160  
  
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175  
  
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly  
180 185 190  
  
Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
420 425

<210> 52  
<211> 1305  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hu-Asp2 (b)  
delta TM

<400> 52  
atggcccaag ccctgccctg gtcctgtcg tggatggcg cggagtgct gcctgcccac 60  
ggcacccagc acggcatccg gtcgcctg cgacggcc tggggggcgc cccctgggg 120  
ctgcggctgc cccggagac cgacgaagag cccgaggagc ccggccggag gggcagctt 180  
gtggagatgg tggacaacct gagggcaag tcggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc ccccgagac gtcacacatc ctggtgata caggcagcag taactttgca 300  
gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtc ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccc acctggtaag catccccat ggccccaacg tcactgtgcg tgccaacatt 480  
gctgccatca ctgaatcaga caagttttc atcaacggct ccaactggga aggcatcctg 540  
gggctggcct atgctgagat tgccaggctt tgtggtgctg gttccccct caaccagtct 600

gaagtgctgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660  
acaggcagtc tctggatac acccatccgg cgggagtggt attatgaggt catcattgtg 720  
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtaaa ctatgacaag 780  
agcattgtgg acagtggcac caccaacctt cggttgcac agaaagtgtt tgaagctgca 840  
gtcaaatcca tcaaggcagc ctcctccacg gagaagttcc ctgatggtt ctggcttagga 900  
gaggcagctgg tgtgctggca agcaggcacc accccttggaa acattttccc agtcatctca 960  
ctctacctaa tgggtgaggt taccaccag tccttcgca tcaccatcct tccgcagcaa 1020  
tacctgcggc cagtggaaaga tgtggccacg tcccaagacg actgttacaa gtttgcac 1080  
tcacagtcat ccacgggcac tggttatggaa gctgttatca tggagggcctt ctacgttg 1140  
tttgcggc cccgaaaaacg aattggctt gctgtcagcg cttgcacatgt gcacgatgag 1200  
ttcaggacgg cagcgggtgga aggccctttt gtcaccccttgg acatggaaga ctgtggctac 1260  
aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

<210> 53

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2 (b)  
delta TM

<400> 53

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly  
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His  
420 425 430

His His

<210> 54  
<211> 2310  
<212> DNA  
<213> Homo sapiens

<400> 54  
atgctgcccg gttggcact gtcctgctg gccgcctgga cggctcgccc gctggaggta 60  
cccaactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120  
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
acctgcattt ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtgcaagac ccattccccac tttgtgattc cctaccgctg cttagttgg 360  
gagtttgtaa gtgatgccct tctcggttcc gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcata ctacggcatg ttgctgccct gcggattga caagttccga 540  
ggggtagagt ttgtgtgttgc cccactggct gaagaaagtgc acaatgtgg 600

gcggaggagg atgactcgga tgcgtggcgg ggcggagcag acacagacta tgcagatggg 660  
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720  
gaagccgatg atgacgagga ccatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
ccctacgaag aagccacaga gagaaccacc agcattcca ccaccaccac caccaccaca 840  
gagtctgtgg aagaggttgt tcgagaggtg tgctctgaac aagccgagac gggccgtgc 900  
cgagcaatga tctcccgctg gtactttat gtgactgaag ggaagtgtgc cccattctt 960  
tacggcggat gtggcggcaa ccggaaacaac tttgacacag aagagtaactg catggccgtg 1020  
tgtggcagcg ccatgtccca aagtttactc aagactaccc aggaacctct tggccgagat 1080  
cctgttaaac ttccataaac agcagccagt acccctgatg ccgttgacaa gtatctcgag 1140  
acacctgggg atgagaatga acatgccat ttccagaaag ccaaagagag gttgaggcc 1200  
aagcaccgag agagaatgtc ccaggtcatg agagaatggg aagaggcaga acgtcaagca 1260  
aagaacttgc ctaaagctga taagaaggca gttatccagc atttccagga gaaagtggaa 1320  
tcttggAAC aggaagcagc caacgagaga cagcagctgg tggagacaca catggccaga 1380  
gtggaagcca tgctcaatga ccggccgcgc ctggccctgg agaactacat caccgctctg 1440  
caggctgttc ctcctcggcc tcgtcacgtg ttcaatatgc taaagaagta tgtcccgca 1500  
gaacagaagg acagacagca caccctaaag catttcgagc atgtgcgcatt ggtgatccc 1560  
aagaaagccg ctcagatccg gtcccaggtt atgacacacc tccgtgtat ttatgagcgc 1620  
atgaatcagt ctctctccct gctctacaac gtgcctgcag tggccgagga gattcaggat 1680  
gaagttgatg agctgcttca gaaagagcaa aactattcag atgacgtt ggcacatg 1740  
attagtgaac caaggatcag ttacggaaac gatgctctca tgccatctt gaccgaaacg 1800  
aaaaccaccg tggagctcct tcccgtgaat ggagagttca gcctggacga tctccagccg 1860  
tggcattctt ttggggctga ctctgtgcca gccaacacag aaaacaaagt tgagcctgtt 1920  
gatccccccc ctgctgcccga ccgaggactg accactcgac caggttctgg gttgacaaat 1980  
atcaagacgg aggagatctc tgaagtgaag atggatgcag aattccgaca tgactcagga 2040  
tatgaagttc atcatcaaaa attgggttca tttgcagaag atgtgggttc aaacaaaggt 2100  
gcaatcattt gactcatggt gggcggtgtt gtcatacgaa cagtgatcgt catcaccttg 2160  
gtgatgctga agaagaaaca gtacacatcc attcatcatg gtgtgggtga gttgacgccc 2220  
gctgtcaccc cagaggagcg ccacctgtcc aagatgcagc agaacggcta cgaaaatcca 2280  
acctacaagt tctttgagca gatgcagaac 2310

<210> 55

<211> 770

<212> PRT

<213> Homo sapiens

<400> 55

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn  
770

<210> 56  
<211> 2253  
<212> DNA  
<213> Homo sapiens

<400> 56

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ctgaacatgc acatgaatgt ccagaatggg aagtggatt cagatccatc agggaccaa 180  
acctgcattg ataccaagga aggcatcctg cagtattgcc aagaagtcta ccctgaactg 240  
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtgcacagac ccataccac tttgtgattc cctaccgctg cttagttgg 360  
gagtttgtaa gtatgcctt tctcggtt gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcacatg ctacggcatg ttgctgcctt gcggattga caagttccga 540  
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ttgggtatgc tgaagaagaa acagtacaca tccattcatc atgggtgggt ggaggttgac 2160  
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ccaaacctaca agttcttga gcagatgcag aac 2253

<210> 57

<211> 751

<212> PRT

<213> Homo sapiens

<400> 57

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg

1

5

10

15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro

20

25

30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln

35

40

45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp

50

55

60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu

65

70

75

80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr  
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu  
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg  
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln  
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe  
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln  
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp  
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val  
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg  
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val  
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met  
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu  
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp  
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn  
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro  
565 570 575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly  
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp  
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg  
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr  
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe  
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe  
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val  
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu  
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp  
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn  
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn  
740 745 750

<210> 58  
<211> 2316  
<212> DNA  
<213> Homo sapiens

<400> 58

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180  
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cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300  
ggccgcaagc agtcaagac ccatccccac tttgtgattc cctaccgctg cttagttgg 360  
gagttgtaa gtgatgcct tctcgccct gacaagtgc aattcttaca ccaggagagg 420  
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagttag 480  
aagagtacca acttgcatac ctacggcatg ttgctgcct gcggatttg caagttccga 540  
gggtagagt ttgtgttgtt cccactggct gaagaaagtg acaatgtgg ttctgctgat 600  
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acctacaagt tcttgagca gatgcagaac aagaag 2316

<210> 59  
<211> 772  
<212> PRT  
<213> Homo sapiens

<400> 59

Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn Lys Lys  
770

<210> 60  
<211> 2259  
<212> DNA  
<213> Homo sapien

<400> 60  
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acgaaaacca ccgtggagct cttcccggtg aatggagagt tcagcctgga cgatctccag 1800  
ccgtggcatt ctttggggc tgactctgtg ccagccaaaca cagaaaacga agttgagcct 1860  
gttcatgccc gccctgctgc cgaccgagga ctgaccactc gaccaggttc tgggttgaca 1920  
aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca 1980  
ggatatgaag ttcatcatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa 2040  
ggtgcaatca ttggactcat ggtggccggt gttgtcatag cgacagtgtat cgtcatcacc 2100  
ttgggtatgc tgaagaagaa acagtacaca tccattcatc atgggttgtt ggaggttgac 2160  
gccgctgtca ccccagagga gcccacactg tccaagatgc agcagaacgg ctacgaaaat 2220  
ccaacctaca agttcttga gcagatgcag aacaagaag 2259

<210> 61  
<211> 753  
<212> PRT  
<213> *Homo sapiens*

<400> 61  
Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15  
  
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30  
  
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45  
  
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60  
  
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80  
  
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95  
  
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110  
  
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125  
  
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140  
  
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160  
  
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175  
  
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190  
  
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205  
  
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220  
  
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240  
  
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255  
  
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270  
  
Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Val Arg  
275 280 285  
  
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300  
  
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr  
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu  
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg  
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln  
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe  
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln  
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp  
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val  
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg  
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val  
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met  
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu  
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp  
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn  
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro  
565 570 575

Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly  
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp  
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg  
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr  
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe  
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe  
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val  
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu  
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp  
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn  
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys  
740 745 750

Lys

<210> 62  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic

<400> 62  
Leu Glu Val Leu Phe Gln Gly Pro  
1 5

<210> 63  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic

<400> 63  
Ser Glu Val Asn Leu Asp Ala Glu Phe Arg  
1 5 10

<210> 64  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic

<400> 64  
Ser Glu Val Lys Met Asp Ala Glu Phe Arg  
1 5 10

<210> 65  
<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 65

Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg  
1 5 10 15

<210> 66

<211> 518

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp  
1 5 10 15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro  
20 25 30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly  
35 40 45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu  
50 55 60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met  
65 70 75 80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met  
85 90 95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly  
100 105 110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr  
115 120 125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp  
130 135 140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu  
145 150 155 160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn  
165 170 175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys  
180 185 190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser  
195 200 205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile  
210 215 220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala  
225 230 235 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro  
245 250 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp  
260 265 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu  
275 280 285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser  
290 295 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val  
305 310 315 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe  
325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp  
340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser  
355 360 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met  
370 375 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro  
385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr  
405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro  
420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe  
435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser  
450 455 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly  
465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys  
485 490 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu  
500 505 510

Val Arg His Arg Trp Lys  
515

<210> 67  
<211> 475  
<212> PRT  
<213> Homo sapiens

<400> 67  
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp  
1 5 10 15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro  
20 25 30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly  
35 40 45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu  
50 55 60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met  
65 70 75 80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met  
85 90 95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly  
100 105 110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr  
115 120 125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp  
130 135 140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu  
145 150 155 160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn  
165 170 175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys  
180 185 190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser  
195 200 205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile  
210 215 220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala  
225 230 235 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro  
245 250 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp  
260 265 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu  
275 280 285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser  
290 295 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val  
305 310 315 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe  
325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp  
340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser  
355 360 365  
Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met  
370 375 380  
Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro  
385 390 395 400  
Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr  
405 410 415  
Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro  
420 425 430  
Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe  
435 440 445  
Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser  
450 455 460  
Glu Pro Ile Leu Trp His His His His His His  
465 470 475

<210> 68  
<211> 413  
<212> PRT  
<213> Homo sapiens

<400> 68  
Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu  
1 5 10 15  
Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu  
20 25 30  
Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp  
35 40 45  
Thr Gly Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile  
50 55 60  
Asp Thr Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly  
65 70 75 80  
Phe Asp Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val  
85 90 95  
Gly Glu Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu  
100 105 110  
Val Asn Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly  
115 120 125  
Ile Lys Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys  
130 135 140  
Pro Ser Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala  
145 150 155 160  
Asn Ile Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro  
165 170 175

Val Ala Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile  
180 185 190

Glu Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu  
195 200 205

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln  
210 215 220

Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val  
225 230 235 240

Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala  
245 250 255

Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp  
260 265 270

Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr  
275 280 285

Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn  
290 295 300

Ser Ser Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln  
305 310 315 320

Pro Met Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile  
325 330 335

Ser Pro Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly  
340 345 350

Phe Tyr Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala  
355 360 365

Ser Pro Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly  
370 375 380

Pro Phe Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser  
385 390 395 400

Leu Ser Glu Pro Ile Leu Trp His His His His His His  
405 410

<210> 69  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 69  
Gly Leu Ala Leu Ala Leu Glu Pro  
1 5

<210> 70  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 70  
Glu Val Lys Met Asp Ala Glu Phe  
1 5

<210> 71  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 71  
Glu Val Asn Leu Asp Ala Glu Phe  
1 5

<210> 72  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 72  
Leu Val Phe Phe Ala Glu Asp Val  
1 5

<210> 73  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 73  
Lys Leu Val Phe Phe Ala Glu Asp  
1 5

<210> 74  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 74  
cgctttaagc ttgccaccat gggcgactg gcccgccg

<210> 75  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 75

cgctttctcg agctaattggt gatggtgatg gtgccacaaa atgggctcgc tcaaaga 57

<210> 76

<211> 15

<212> PRT

<213> Artificial Sequence

*Sub B6*

<223> Description of Artificial Sequence: Peptide

<400> 76

Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg  
1 5 10 15

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*Sub B6  
Concluded*